SEQUENCE LISTING

<110> HERMONAT, Paul L.

<120> ADENO-ASSOCIATED VIRUS AAV REP78 MAJOR REGULATORY PROTEIN, MUTANTS
 THEREOF AND USES THEREOF

<130> 023533/0130

<140> US 09/693,908
<141> 2000-10-23

<150> US 60/160,608
<151> 1999-10-21

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<170> PatentIn version 3.1

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<223> Primer

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gccaactcca tcactagggg ttcctggagg ggtggagtcg tgacgtgaat tacgtcatag   180

ggttagggag gtcctgtatt agaggtcacg tgagtgtttt gcgacatttt gcgacaccat   240

gtggtcacgc tgggtattta gcccgagtg agcacgcagg tctccattt tgaagcggga   300

ggtttgaacg cgcagccgcc atg ccg ggg ttt tac gag att gtg att aag gtc   353
                       Met Pro Gly Phe Tyr Glu Ile Val Ile Lys Val
                        1   5   10

ccc agc gac ctt gac ggg cat ctg ccc ggc att tct gac agc ttt gtg   401
Pro Ser Asp Leu Asp Gly His Leu Pro Gly Ile Ser Asp Ser Phe Val
            15   20   25

aac tgg gtg gcc gag aag gaa tgg gag ttg ccg cca gat tct gac atg   449
Asn Trp Val Ala Glu Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met
        30   35   40

gat ctg aat ctg att gag cag gca ccc ctg acc gtg gcc gag aag ctg   497
Asp Leu Asn Leu Ile Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu
    45   50   55

cag cgc gac ttt ctg acg gaa tgg cgc cgt gtg agt aag gcc ccg gag   545
Gln Arg Asp Phe Leu Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu
60   65   70   75

gcc ctt ttc ttt gtg caa ttt gag aag gga gag agc tac ttc cac atg   593
Ala Leu Phe Phe Val Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met
                80   85   90

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cac gtg ctc gtg gaa acc acc ggg gtg aaa tcc atg gtt ttg gga cgt        641
His Val Leu Val Glu Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg
                95                  100              105

ttc ctg agt cag att cgc gaa aaa ctg att cag aga att tac cgc ggg        689
Phe Leu Ser Gln Ile Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly
            110              115              120

atc gag ccg act ttg cca aac tgg ttc gcg gtc aca aag acc aga aat        737
Ile Glu Pro Thr Leu Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn
        125              130              135

ggc gcc gga ggc ggg aac aag gtg gtg gat gag tgc tac atc ccc aat        785
Gly Ala Gly Gly Gly Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn
140              145              150              155

tac ttg ctc ccc aaa acc cag cct gag ctc cag tgg gcg tgg act aat        833
Tyr Leu Leu Pro Lys Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn
                160              165              170

atg gaa cag tat tta agc gcc tgt ttg aat ctc acg gag cgt aaa cgg        881
Met Glu Gln Tyr Leu Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg
                175              180              185

ttg gtg gcg cag cat ctg acg cac gtg tcg cag acg cag gag cag aac        929
Leu Val Ala Gln His Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn
            190              195              200

aaa gag aat cag aat ccc aat tct gat gcg ccg gtg atc aga tca aaa        977
Lys Glu Asn Gln Asn Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys
        205              210              215

act tca gcc agg tac atg gag ctg gtc ggg tgg ctc gtg gac aag ggg       1025
Thr Ser Ala Arg Tyr Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly
220              225              230              235

att acc tcg gag aag cag tgg atc cag gag gac cag gcc tca tac atc       1073
Ile Thr Ser Glu Lys Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile
            240              245              250

tcc ttc aat gcg gcc tcc aac tcg cgg tcc caa atc aag gct gcc ttg       1121
Ser Phe Asn Ala Ala Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu
            255              260              265

gac aat gcg gga aag att atg agc ctg act aaa acc gcc ccc gac tac       1169
Asp Asn Ala Gly Lys Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr
        270              275              280

ctg gtg ggc cag cag ccc gtg gag gac att tcc agc aat cgg att tat       1217
Leu Val Gly Gln Gln Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr
        285              290              295

aaa att ttg gaa cta aac ggg tac gat ccc caa tat gcg gct tcc gtc       1265
Lys Ile Leu Glu Leu Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val
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ttt ctg gga tgg gcc acg aaa aag ttc ggc aag agg aac acc atc tgg      1313
Phe Leu Gly Trp Ala Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp
            320             325             330

ctg ttt ggg cct gca act acc ggg aag acc aac atc gcg gag gcc ata      1361
Leu Phe Gly Pro Ala Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile
            335             340             345

gcc cac act gtg ccc ttc tac ggg tgc gta aac tgg acc aat gag aac      1409
Ala His Thr Val Pro Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn
            350             355             360

ttt ccc ttc aac gac tgt gtc gac aag atg gtg atc tgg tgg gag gag      1457
Phe Pro Phe Asn Asp Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu
            365             370             375

ggg aag atg acc gcc aag gtc gtg gag tcg gcc aaa gcc att ctc gga      1505
Gly Lys Met Thr Ala Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly
380             385             390             395

gga agc aag gtg cgc gtg gac cag aaa tgc aag tcc tcg gcc cag ata      1553
Gly Ser Lys Val Arg Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile
            400             405             410

gac ccg act ccc gtg atc gtc acc tcc aac acc aac atg tgc gcc gtg      1601
Asp Pro Thr Pro Val Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val
            415             420             425

att gac ggg aac tca acg acc ttc gaa cac cag cag ccg ttg caa gac      1649
Ile Asp Gly Asn Ser Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp
            430             435             440

cgg atg ttc aaa ttt gaa ctc acc cgc cgt ctg gat cat gac ttt ggg      1697
Arg Met Phe Lys Phe Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly
            445             450             455

aag gtc acc aag cag gaa gtc aaa gac ttt ttc cgg tgg gca aag gat      1745
Lys Val Thr Lys Gln Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp
460             465             470             475

cac gtg gtt gag gtg gag cat gaa ttc tac gtc aaa aag ggt gga gcc      1793
His Val Val Glu Val Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala
            480             485             490

aag aaa aga ccc gcc ccc agt gac gca gat ata agt gag ccc aaa cgg      1841
Lys Lys Arg Pro Ala Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg
            495             500             505

gtg cgc gag tca gtt gcg cag cca tcg acg tca gac gcg gaa gct tcg      1889
Val Arg Glu Ser Val Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser
            510             515             520

atc aac tac gca gac agg tac caa aac aaa tgt tct cgt cac gtg ggc      1937
Ile Asn Tyr Ala Asp Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly
            525             530             535
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atg aat ctg atg ctg ttt ccc tgc aga caa tgc gag aga atg aat cag     1985
Met Asn Leu Met Leu Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln
540                 545                 550                 555

aat tca aat atc tgc ttc act cac gga cag aaa gac tgt tta gag tgc     2033
Asn Ser Asn Ile Cys Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys
                    560                 565                 570

ttt ccc gtg tca gaa tct caa ccc gtt tct gtc gtc aaa aag gcg tat     2081
Phe Pro Val Ser Glu Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr
                    575                 580                 585

cag aaa ctg tgc tac att cat cat atc atg gga aag gtg cca gac gct     2129
Gln Lys Leu Cys Tyr Ile His His Ile Met Gly Lys Val Pro Asp Ala
            590                 595                 600

tgc act gcc tgc gat ctg gtc aat gtg gat ttg gat gac tgc atc ttt     2177
Cys Thr Ala Cys Asp Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe
            605                 610                 615

gaa caa taaatgattt aaatcaggta tggctgccga tggttatctt ccagattggc     2233
Glu Gln
620


tcgaggacac tctctctgaa ggaataagac agtggtggaa gctcaaacct ggcccaccac     2293

caccaaagcc cgcagagcgg cataaggacg acagcagggg tcttgtgctt cctgggtaca     2353

agtacctcgg acccttcaac ggactcgaca agggagagcc ggtcaacgag gcagacgccg     2413

cggccctcga gcacgtacaa agcctacgac cggcagctcg acagcggaga caacccgtac     2473

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ttttcaccac gtgactggca agactcatc aacaacaact ggggattccg acccaagaga     3133

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40

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atggtgccac agtatggata cctcaccctg aacaacggga gtcaggcagt aggacgctct    3373

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aatggcagag actctctggt gaatccggcc atggcaagcc acaaggacga tgaagaaaag    3793

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Lys Glu Trp Glu Leu Pro Pro Asp Ser Asp Met Asp Leu Asn Leu Ile
            35   40   45

Glu Gln Ala Pro Leu Thr Val Ala Glu Lys Leu Gln Arg Asp Phe Leu
        50   55   60

Thr Glu Trp Arg Arg Val Ser Lys Ala Pro Glu Ala Leu Phe Phe Val
65   70   75   80

Gln Phe Glu Lys Gly Glu Ser Tyr Phe His Met His Val Leu Val Glu
                85   90   95

Thr Thr Gly Val Lys Ser Met Val Leu Gly Arg Phe Leu Ser Gln Ile
            100   105   110

Arg Glu Lys Leu Ile Gln Arg Ile Tyr Arg Gly Ile Glu Pro Thr Leu
        115   120   125

Pro Asn Trp Phe Ala Val Thr Lys Thr Arg Asn Gly Ala Gly Gly Gly
    130   135   140

Asn Lys Val Val Asp Glu Cys Tyr Ile Pro Asn Tyr Leu Leu Pro Lys
145   150   155   160

Thr Gln Pro Glu Leu Gln Trp Ala Trp Thr Asn Met Glu Gln Tyr Leu
                165   170   175

Ser Ala Cys Leu Asn Leu Thr Glu Arg Lys Arg Leu Val Ala Gln His
            180   185   190

Leu Thr His Val Ser Gln Thr Gln Glu Gln Asn Lys Glu Asn Gln Asn
            195   200   205

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1

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Pro Asn Ser Asp Ala Pro Val Ile Arg Ser Lys Thr Ser Ala Arg Tyr
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Met Glu Leu Val Gly Trp Leu Val Asp Lys Gly Ile Thr Ser Glu Lys
225              230              235              240

Gln Trp Ile Gln Glu Asp Gln Ala Ser Tyr Ile Ser Phe Asn Ala Ala
            245              250              255

Ser Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Gly Lys
        260              265              270

Ile Met Ser Leu Thr Lys Thr Ala Pro Asp Tyr Leu Val Gly Gln Gln
        275              280              285

Pro Val Glu Asp Ile Ser Ser Asn Arg Ile Tyr Lys Ile Leu Glu Leu
    290              295              300

Asn Gly Tyr Asp Pro Gln Tyr Ala Ala Ser Val Phe Leu Gly Trp Ala
305              310              315              320

Thr Lys Lys Phe Gly Lys Arg Asn Thr Ile Trp Leu Phe Gly Pro Ala
            325              330              335

Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
        340              345              350

Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
        355              360              365

Cys Val Asp Lys Met Val Ile Trp Trp Glu Glu Gly Lys Met Thr Ala
    370              375              380

Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
385              390              395              400

Val Asp Gln Lys Cys Lys Ser Ser Ala Gln Ile Asp Pro Thr Pro Val
            405              410              415

Ile Val Thr Ser Asn Thr Asn Met Cys Ala Val Ile Asp Gly Asn Ser
        420              425              430
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Thr Thr Phe Glu His Gln Gln Pro Leu Gln Asp Arg Met Phe Lys Phe
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Glu Leu Thr Arg Arg Leu Asp His Asp Phe Gly Lys Val Thr Lys Gln
        450             455             460

Glu Val Lys Asp Phe Phe Arg Trp Ala Lys Asp His Val Val Glu Val
465             470             475             480

Glu His Glu Phe Tyr Val Lys Lys Gly Gly Ala Lys Lys Arg Pro Ala
                485             490             495

Pro Ser Asp Ala Asp Ile Ser Glu Pro Lys Arg Val Arg Glu Ser Val
            500             505             510

Ala Gln Pro Ser Thr Ser Asp Ala Glu Ala Ser Ile Asn Tyr Ala Asp
        515             520             525

Arg Tyr Gln Asn Lys Cys Ser Arg His Val Gly Met Asn Leu Met Leu
        530             535             540

Phe Pro Cys Arg Gln Cys Glu Arg Met Asn Gln Asn Ser Asn Ile Cys
545             550             555             560

Phe Thr His Gly Gln Lys Asp Cys Leu Glu Cys Phe Pro Val Ser Glu
                565             570             575

Ser Gln Pro Val Ser Val Val Lys Lys Ala Tyr Gln Lys Leu Cys Tyr
            580             585             590

Ile His His Ile Met Gly Lys Val Pro Asp Ala Cys Thr Ala Cys Asp
        595             600             605

Leu Val Asn Val Asp Leu Asp Asp Cys Ile Phe Glu Gln
    610             615             620
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